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(p27 [Kip1])

1	ATGTCAAACGTGCGAGTGTCTAACGGGAGCCCTAGCCTGGAGCGG
	MetSerAsnValArgValSerAsnGlySerProSerLeuGluArg
46	ATGGACGCCAGGCAGGCGGAGCACCCCAAGCCCTCGGCCTGCAGG
	MetAspAlaArgGlnAlaGluHisProLysProSerAlaCysArg
91	AACCTCTTCGGCCCGGTGGACCACGAAGAGTTAACCCGGGACTTG
	AsnLeuPheGlyProValAspHisGluGluLeuThrArgAspLeu
136	GAGAAGCACTGCAGAGACATGGAAGAGGCGAGCCAGCGCAAGTGG
	GluLysHisCysArgAspMetGluGluAlaSerGlnArgLysTrp
181	AATTTCGATTTTCAGAATCACAAACCCCTAGAGGGCAAGTACGAG
	AsnPheAspPheGlnAsnHisLysProLeuGluGlyLysTyrGlu
226	TGGCAAGAGGTGGAGAAGGGCAGCTTGCCCGAGTTCTACTACAGA
	TrpGlnGluValGluLysGlySerLeuProGluPheTyrTyrArg
271	CCCCCGCGCCCCCAAAGGTGCCTGCAAGGTGCCGGCGCAGGAG
	ProProArgProProLysGlyAlaCysLysValProAlaGlnGlu
316	AGCCAGGATGTCAGCGGGAGCCGCCCGGCGCGCCCTTTAATTGGG
	SerGlnAspValSerGlySerArgProAlaAlaProLeuIleGly
361	GCTCCGGCTAACTCTGAGGACACGCATTTGGTGGACCCAAAGACT
	AlaProAlaAsnSerGluAspThrHisLeuValAspProLysThr
406	GATCCGTCGGACAGCCAGACGGGGTTAGCGGAGCAATGCGCAGGA
	AspProSerAspSerGlnThrGlyLeuAlaGluGlnCysAlaGly
451	ATAAGGAAGCGACCTGCAACCGACGATTCTTCTACTCAAAACAAA
	IleArgLysArgProAlaThrAspAspSerSerThrGlnAsnLys
496	AGAGCCAACAGAACAGAAGAAAATGTTTCAGACGGTTCCCCAAAT
	ArgAlaAsnArgThrGluGluAsnValSerAspGlySerProAsn
541	GCCGGTTCTGTGGAGCAGACGCCCAAGAAGCCTGGCCTCAGAAGA
	AlaGlySerValGluGlnThrProLysLysProGlyLeuArgArg
586	CGTCAAACGTAA
	ArgGlnThr

Fig. 1

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FKBP-12 SEQUENCE

GlyArgThrPheProLysArgGlyGlnThrCysValValHisTy 91 ACCGGGATGCTTGAAGATGGAAAGAAATTTGATTCCTCCCGGGA ThrGlyMetLeuGluAspGlyLysLysPheAspSerSerArgAs 136 AGAAACAAGCCCTTTAAGTTTATGCTAGGCAAGCAGGAGGTGAT ArgAsnLysProPheLysPheMetLeuGlyLysGlnGluValII 181 CGAGGCTGGGAAGAAGGGGTTGCCCAGATGAGTGTGGGTCAGAG ArgGlyTrpGluGluGlyValAlaGlnMetSerValGlyGlnAr 226 GCCAAACTGACTATATCTCCAGATTATGCCTATGGTGCCACTGG AlaLysLeuThrIleSerProAspTyrAlaTyrGlyAlaThrGl 271 CACCCAGGCATCATCCCACCACATGCCACTCTCGTCTTCGATGT HisProGlyIleIleProProHisAlaThrLeuValPheAspVa 316 GAGCTTCTAAAACTGGAATGACAGGAATGGCCTCCCCTTAGC GluLeuLeuLysLeuGlu 361 CCCTGTTCTTGGATCTGCCTGGAGGGATCTGGTGCCTCCAGACA 406 GTGCACATGATCCATATGGAGCTTTTCCTGATGTTCCACTCACA 451 TTGTATAGACATCTGCCTTGATTTCCTCTTCTCTCTCTCT	1	GCCGCCGCCATGGGAGTGCAGGTGGAAACCATCTCCCCAGGAGAC MetGlyValGlnValGluThrIleSerProGlyAsp
ThrGlyMetLeuGluAspGlyLysLysPheAspSerSerArgAs AGAAACAAGCCCTTTAAGTTTATGCTAGGCAAGCAGGAGGTGAT ArgAsnLysProPheLysPheMetLeuGlyLysGlnGluValII CGAGGCTGGGAAGAAGGGGTTGCCCAGATGAGTGTGGGTCAGAGATGGIYTrpGluGluGlyValAlaGlnMetSerValGlyGlnAr CGAGGCTGACCTATATCTCCAGATTATGCCTATGGTGCCACTGGAIALLYSLeuThrIleSerProAspTyrAlaTyrGlyAlaThrGl CACCCAGGCATCATCCCACCACATGCCACTCTCGTCTTCGATGTHisProGlyIleIleProProHisAlaThrLeuValPheAspVal GAGCTTCTAAAACTGGAATGACAGGAATGGCCTCCTCCCTTAGCGILLeuLeuLysLeuGlu CCCTGTTCTTGGATCTGCCTGGAGGGATCTGGTGCCTCCAGACAGGACATGACACATGACACATGACCACTTTCTCTCATGTTCCACTCACCACATGCCACATGATCTAGACATGATCCATCAGCACATGTTCTCTCACTCA	46	GGGCGCACCTTCCCCAAGCGCGGCCAGACCTGCGTGGTGCACTACGLyArgThrPheProLysArgGlyGlnThrCysValValHisTyr
ArgAsnLysProPheLysPheMetLeuGlyLysGlnGluValII CGAGGCTGGGAAGAAGGGGTTGCCCAGATGAGTGTGGGTCAGAGATGAGTTTPGLuGluGlyValAlaGlnMetSerValGlyGlnAr CGCAAACTGACTATATCTCCAGATTATGCCTATGGTGCCACTGGALALysLeuThrIleSerProAspTyrAlaTyrGlyAlaThrGl CACCCAGGCATCATCCCACCACATGCCACTCTCGTCTTCGATGTHisProGlyIleIleProProHisAlaThrLeuValPheAspValGluLeuLeuLysLeuGlu GAGCTTCTAAAACTGGAATGACAGGAATGGCCTCCTCCCTTAGGGIULeuLeuLysLeuGlu CCCTGTTCTTGGATCTGCCTGGAGGGATCTGGTGCCTCCAGACAGGGACATGACATGACATGACATGACATGACATGACATGACATGACATGATGTTCCACTCCAGACAGA	91	ACCGGGATGCTTGAAGATGGAAAGAAATTTGATTCCTCCCGGGACThrGlyMetLeuGluAspGlyLysLysPheAspSerSerArgAsp
ArgGlyTrpGluGluGlyValAlaGlnMetSerValGlyGlnAr 226 GCCAAACTGACTATATCTCCAGATTATGCCTATGGTGCCACTGG AlaLysLeuThrIleSerProAspTyrAlaTyrGlyAlaThrGl 271 CACCCAGGCATCATCCCACCACATGCCACTCTCGTCTTCGATGT HisProGlyIleIleProProHisAlaThrLeuValPheAspVa 316 GAGCTTCTAAAACTGGAATGACAGGAATGGCCTCCTCCCTTAGC GluLeuLeuLysLeuGlu 361 CCCTGTTCTTGGATCTGCCTGGAGGGATCTGGTGCCTCCAGACA 406 GTGCACATGATCCATATGGAGCTTTTCCTGATGTTCCACTCCAC 451 TTGTATAGACATCTGCCTGTTTCCTCTTTCTCCTCGTAT	136	AGAAACAAGCCCTTTAAGTTTATGCTAGGCAAGCAGGAGGTGATCATGASNLysProPheLysPheMetLeuGlyLysGlnGluValIle
AlaLysLeuThrIleSerProAspTyrAlaTyrGlyAlaThrGl CACCCAGGCATCATCCCACCACATGCCACTCTCGTCTTCGATGT HisProGlyIleIleProProHisAlaThrLeuValPheAspVa GAGCTTCTAAAACTGGAATGACAGGAATGGCCTCCTCCCTTAGC GluLeuLeuLysLeuGlu CCCTGTTCTTGGATCTGCCTGGAGGGATCTGGTGCCTCCAGACA GTGCACATGATCCATATGGAGCTTTTCCTGATGTTCCACTCCAC TTGTATAGACATCTGCCCTGACTGAATGTGTTCTGTCACTCAGC TTGCTTCCGACACCCTCTGTTTCCTCTCCCCTTTCTCCTCGTAT	181	CGAGGCTGGGAAGAAGGGGTTGCCCAGATGAGTGTGGGTCAGAGA ArgGlyTrpGluGluGlyValAlaGlnMetSerValGlyGlnArg
HisProGlyIleIleProProHisAlaThrLeuValPheAspVa GAGCTTCTAAAACTGGAATGACAGGAATGGCCTCCTCCCTTAGC GluLeuLeuLysLeuGlu CCCTGTTCTTGGATCTGCCTGGAGGGATCTGGTGCCTCCAGACA GTGCACATGATCCATATGGAGCTTTTCCTGATGTTCCACTCCAC TTGTATAGACATCTGCCCTGACTGAATGTGTTCTGTCACTCAGC TTGCTTCCGACACCCTCTGTTTCCTCTCCCCTTTCTCCTCGTAT	226	GCCAAACTGACTATATCTCCAGATTATGCCTATGGTGCCACTGGGALaLysLeuThrIleSerProAspTyrAlaTyrGlyAlaThrGly
GluLeuLysLeuGlu 361 CCCTGTTCTTGGATCTGCCTGGAGGGATCTGGTGCCTCCAGACA 406 GTGCACATGATCCATATGGAGCTTTTCCTGATGTTCCACTCCAC 451 TTGTATAGACATCTGCCCTGACTGAATGTGTTCTGTCACTCAGC 496 TTGCTTCCGACACCTCTGTTTCCTCTTCCCCTTTCTCCTCGTAT	271	CACCCAGGCATCATCCCACCACATGCCACTCTCGTCTTCGATGTGHISProGlyIleIleProProHisAlaThrLeuValPheAspVal
406 GTGCACATGATCCATATGGAGCTTTTCCTGATGTTCCACTCCAC 451 TTGTATAGACATCTGCCCTGACTGAATGTGTTCTGTCACTCAGC 496 TTGCTTCCGACACCTCTGTTTCCTCTTCCCCTTTCTCCTCGTAT	316	GAGCTTCTAAAACTGGAATGACAGGAATGGCCTCCTCCCTTAGCTGluLeuLeuLysLeuGlu
- 5 Δ. Τα Τη Τα Τη Τα Το	406 451	CCCTGTTCTTGGATCTGCCTGGAGGGATCTGGTGCCTCCAGACAT GTGCACATGATCCATATGGAGCTTTTCCTGATGTTCCACTCCACT TTGTATAGACATCTGCCCTGACTGAATGTGTTCTGTCACTCAGCT TTGCTTCCGACACCTCTGTTTCCTCTTCCCCTTTCTCCTCGTATG TGTGTTTACCTAAACTATATGCCATAAACCTCAAGTTATTCA

Fig. 2





DEMONSTRATION OF THE P27(KIP1):FKBP12 INTERACTION

	P27(Kip1)	Αl	B1
CDK2	+	-	-
FKBP-12	+		-
TRK	-	-	-
CYC-B	_	-	_
Vector	-	-	_

Fig. 3